

cDNA original library A or B of certain normal tissue or typical pathological tissue
(designated as A original library, B original library)



Constructing several homogenized libraries with $C_o t \leq 1$ so that the high abundance cDNA can be enriched in the column (corresponding to the first class of mRNA). Collecting and translating to several highly repeated homogenized cDNA libraries, respectively. (designated as: A⁺⁺⁺. B⁺⁺⁺.....).



Collecting elution peak



Constructing several homogenized libraries with $1 \leq C_o t \leq 50$ so that moderate abundance cDNA libraries can be enriched in the column (corresponding to the second class of mRNA). Collecting and converting them into several moderately repeated homogenized cDNA libraries, respectively. (designated as: A⁺⁺. B⁺⁺.....).



Collecting elution peak



Constructing several homogenized libraries with $C_o t \geq 50$ so that low abundance or rare homogenized cDNA libraries may be obtained after collecting and converting, (corresponding to the third class of mRNA), (designated as: A⁺. B⁺.....).

Figure 1

Subtracting homogenized A^{+++} according to the introduced method of subtraction



Constructing several homogenized sublibraries with $C_o t \leq 1$ so that the highly expressed cDNAs in A, B, C.....can be enriched in the column, and those in elution peak are the high abundance cDNAs that only express in A. They are designated as: spA_1^{+++} . spA_2^{+++}



Similarly, homogenizing library A^{++} with $1 \leq C_o t \leq 50$ so that homogenized sublibraries that contains the moderate abundance cDNA only expressed in A can be obtained in elution peak. They are designated as: spA_1^{++} . spA_2^{++}



Similarly, homogenizing library A^+ when $C_o t \geq 1-50$ so that homogenized libraries that contains the low abundance or rare cDNA only expressed in A can be obtained in elution peak. They are designated as: spA_1^+ . spA_2^+

Figure 2

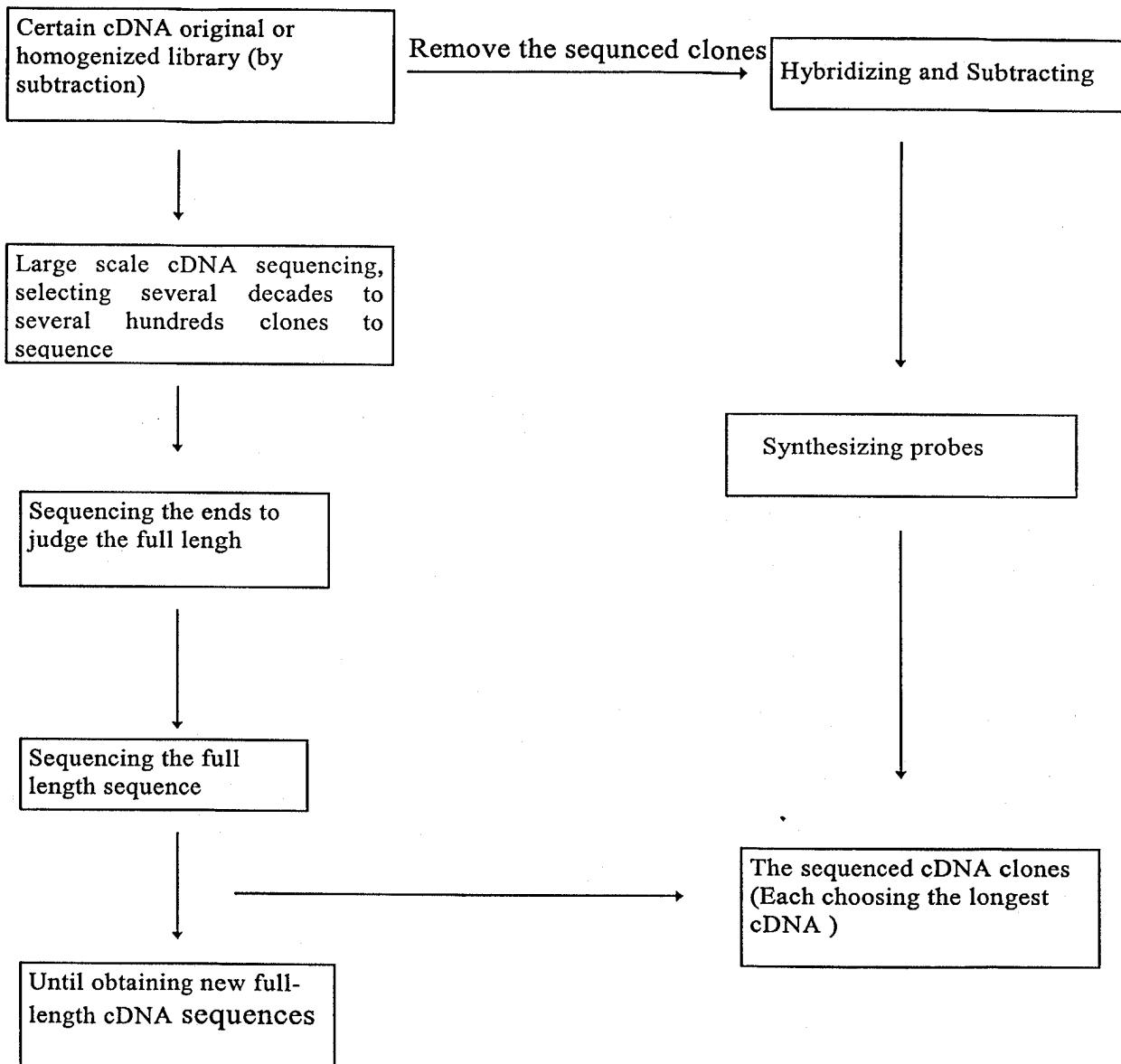


Figure 3